

SEQUENCE LISTING

<110> Tang et al.

<120> METHODS AND MATERIALS RELATING TO NOVEL STEM CELL GROWTH FACTOR-LIKE POLYPEPTIDES AND POLYNUCLEOTIDES

<130> 28110/37260

<140>

<141> 2001-06-28

<150> To be assigned

<151> 2001-04-05

<150> 60/266,614

<151> 2001-02-05

<150> 60/215,733

<151> 2000-06-28

<150> 09/757,562

<151> 2001-01-09

<150> 09/543,774

<151> 2000-04-05

<160> 48

<170> PatentIn version 3.0

<210> 1

<211> 301

<212> DNA

<213> Homo sapiens

<400> 1

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gagaaaacaa acagcagcag aagaagcga aagtccaaga taaacagaaa tcggtatcag 180

tcagcactgt acactagagg gttccatgag attattgtag actcatgatg ctgctatctc 240

aaccagatgc ccaggacagg tgctctagcc attaggacca caaatggaca tgtcagttat 300

t 301

<210> 2

<211> 392

<212> DNA

<213> Homo sapiens

<400> 2

09894912.062801

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 ccttgacaat tgcccagaag ggttggaaagc caacaaccat actatggagt gtgtcagtat 180
 tgtgcactgt gaggtcagtg aatggaatcc ttggagtcca tgcacgaaga agggaaaaac 240
 atgtggcttc aaaagaggga ctgaaacacg ggtccgagaa ataatacagc atccttcagc 300
 aaagggtaac ctatgtcccc caacaaatga gacaagaaag tgtacagtgc aaaggaagaa 360
 gtgtcagaag ggagaacgag gaaaataagg ag 392

<210> 3
 <211> 475
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> misc_feature
 <222> (1)..(475)
 <223> n = A, T, G, or C

<400> 3
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 ccacgcgtnc gcccacgcgt cccgagagga aaagaaaaaa acctaattta ggagaaagta 120
 aagaagcaat acctgacagc ggaagtctgg aatggagcaa agaaatccca gagcaacgag 180
 aaaacaaaca gcagcagaag aagcgaaaag tccaagataa acagaaatcg gtatcagtca 240
 gcactgtaca ctagagggtt ccatgagatt attgtagact catgatgctg ctatctcaac 300
 cagatgccca ggacaggtgc tctagccatt aggaccacaa atggacatgt cagttattgc 360
 tctgtctaaa caacattccc agtagttgct atattcttca tacaagcata gttaacaaca 420
 aagagccaaa agatcaaaga agggatactt tcagatgggt gtcttgtgtg cttcn 475

<210> 4
 <211> 473
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> misc_feature
 <222> (1)..(473)
 <223> n = A, T, G, or C

<400> 4
 tgggcannnn aaanttttga nattcgatcc gcgctgcagg aattcggcac gagacgagga 60
 aaaaaaggaa gggagaggaa aagaaaaaaa cctaataaag gagaaagtaa agaagcaata 120
 cctgacagca aaagtctgga atccagcaga gaaatcccag agcaacgaga aaacaaacag 180

cagcagaaga agcgaaaagt ccaagataaa cagaaatcgg tatcagtcag cactgtacac 240
tagaggggttc catgagatta ttgtagactc atgatgctgc tatctcaacc agatgcccag 300
gacaggtgct ctagccatta ggaccacaaa tggacatgtc agttattgct ctgtctaaac 360
aacattccca gtagttgcta tattcttcat acaagcatag ttaacaacaa agagccaaaa 420
gatcaaagaa gggatacttt cagatgggtg tcttgtgtgc ttctctgcat ttt 473

<210> 5
<211> 462
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(462)
<223> n = A, T, G, or C

<400> 5
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agggaaagaa aaaaacctaa taaaggagaa agtaaagaat caatttctga cagcaaaagt 120
ctggaatcca tcaaagaaat cccatatcaa cgagaaaaca gacagcagca caaaaagcga 180
aaagtccaag ataaacagaa atcgggtatca gtcagcactg tacactagag gggtccatga 240
gattattgta gactcatgat gctgctatct caaccagatg cccaggacag gtgctctatc 300
cattacgacc acaaatggac atgtcagtta ttgctctgtc taaacaacat tcccagtagt 360
tgctatatcc ttcatacaag catagttaac aacaaagagc caaaagatca aagaagggat 420
actttcagat gggtgtcttg tgtgcttctc tgcattttta aa 462

<210> 6
<211> 384
<212> DNA
<213> Homo sapiens

<400> 6
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aaaatgtaaa agtggatttt acttacacct tggaaagtgc cttgacaatt gccagaagg 120
gttggaagcc aacaaccata ctatggagtg tgtcagtatt gtgcactgtg aggtcagtga 180
atggaatcct tggagtccat gcacgaagaa gggaaaaaca tgtggcttca aaagagggac 240
tgaaacacgg gtccgagaaa taatacagca tccttcagca aagggttaacc tatgtcccc 300
aacaatgag acaagaaagt gtacagtgc aaggaagaag tgtcagaagg gagaacgagg 360
aaaaaaagga agggagagga aaag 384

<210> 7
 <211> 390
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature

 <222> (1)..(390)
 <223> n = A, T, G, or C

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 ctttctcctt tattagggtt ttttcttttc ctctcccttc ctttttttcc tcgttctccc 120
 ttctgacact tcttcctttg cactgtacac tttcttgtct catttggttg gggacatagg 180
 ttaccctttg ctgaaggatg ctgtattatt tctcggaccc gtgtttcagt ccctcttttg 240
 aagccacatg tttttccctt cttcgtgcat ggactccaag gattccattc actgacctca 300
 cagtgcacaa tactgacaca ctccatagta tgggtgttg cttccaaccc ttctgggcaa 360
 ttgtcaaggc actttccaag gtgtaagtan 390

<210> 8
 <211> 1345
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature

 <222> (321)..(1235)
 <223> similar to gi4519541 in the genpept database release 114, Run with FASTXY3.3t00, default parameter

<400> 8
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 gccgcgcgag ttcagtgtt ggataatttg aaagtacaat agttggttcc cctgtccacc 120
 cgccccactt cgtttgccat cacagcacgc ctatcggatg tgagaggaga agtcccgtg 180
 ctcgggcact gtctatatac gcctaacacc tacatatatt ttaaaaacat taaatataat 240
 taacaatcaa aagaaagagg agaaaggaag ggaagcatta ctgggttact atgcacttgc 300
 gactgatttc ttggcttttt atcattttga actttatgga atacatcggc agccaaaacg 360
 cctcccgggg aaggcgccag cgaagaatgc atcctaacgt tagtcaaggc tgccaaggag 420
 gctgtgcaac atgtctcagat tacaatggat gtttgtcatg taagcccaga ctattttttg 480
 ctctggaaaag aattggcatg aagcagattg gagtatgtct catcttcatg tccaagtgga 540
 tattatggaa ctcgatatcc agatataaat aatgtgtaca aaatgcaaag ctgactgtga 600
 tacctgtttc aacaaaaatt tctgcacaaa atgtaaaagt ggattttact tacaccttgg 660

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aaagtgcctt gacaattgcc cagaagggtt ggaagccaac aaccatacta tggagtgtgt 720
cagtattgtg cactgtgagg tcagtgaatg gaatccttgg agtccatgca cgaagaaggg 780
aaaaacatgt ggcttcaaaa gagggactga aacacgggtc cgagaaataa tacagcatcc 840
ttcagcaaag ggtaacctat gtcccccaac aaatgagaca agaaagtgtg cagtgcaaag 900
gaagaagtgt cagaaggggag aacgaggaaa aaaaggaagg gagaggaaaa gaaaaaaacc 960
taataaagga gaaagtaaag aagcaatacc tgacagcaaa agtctggaat ccagcaaaga 1020
aatcccagag caacgagaaa acaaacagca gcagaagaag cgaaaagtcc aagataaaca 1080
gaaatcggta tcagtcagca ctgtacacta gagggttcca tgagattatt gtagactcat 1140
gatgctgcta tctcaaccag atgcccagga caggtgctct agccattagg accacaaatg 1200
gacatgtcag ttattgctct gtctaaacaa cattcccagt agttgctata ttcttcatac 1260
aagcatagtt aacaacaaag agccaaaaga tcaaagaagg gatactttca gatgggtgtc 1320
ttgtgtgctt ctctgcattt ttaaa 1345

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<210> 9
<211> 1343
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (291)..(1109)

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cgccccactt cgcttgccat cacagcacgc ctatcggatg tgagaggaga agtcccgtg 180
ctcgggcact gtctatatac gcctaacacc tacatatatt ttaaaaacat taaatataat 240
taacaatcaa aagaaagagg agaaaggaag ggaagcatta ctgggttact atg cac 296
                                     Met His
                                     1

ttg cga ctg att tct tgg ctt ttt atc att ttg aac ttt atg gaa tac 344
Leu Arg Leu Ile Ser Trp Leu Phe Ile Ile Leu Asn Phe Met Glu Tyr
      5                      10                      15

atc ggc agc caa aac gcc tcc cgg gga agg cgc cag cga aga atg cat 392
Ile Gly Ser Gln Asn Ala Ser Arg Gly Arg Arg Gln Arg Arg Met His
      20                      25                      30

cct aac gtt agt caa ggc tgc caa gga ggc tgt gca aca tgc tca gat 440
Pro Asn Val Ser Gln Gly Cys Gln Gly Gly Cys Ala Thr Cys Ser Asp
      35                      40                      45                      50

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tac	aat	gga	tgt	ttg	tca	tgt	aag	ccc	aga	cta	ttt	ttt	gct	ctg	gaa	488
Tyr	Asn	Gly	Cys	Leu	Ser	Cys	Lys	Pro	Arg	Leu	Phe	Phe	Ala	Leu	Glu	
			55						60					65		
aga	att	ggc	atg	aag	cag	att	gga	gta	tgt	ctc	tct	tca	tgt	cca	agt	536
Arg	Ile	Gly	Met	Lys	Gln	Ile	Gly	Val	Cys	Leu	Ser	Ser	Cys	Pro	Ser	
			70					75					80			
gga	tat	tat	gga	act	cga	tat	cca	gat	ata	aat	aag	tgt	aca	aaa	tgc	584
Gly	Tyr	Tyr	Gly	Thr	Arg	Tyr	Pro	Asp	Ile	Asn	Lys	Cys	Thr	Lys	Cys	
		85					90					95				
aaa	gct	gac	tgt	gat	acc	tgt	ttc	aac	aaa	aat	ttc	tgc	aca	aaa	tgt	632
Lys	Ala	Asp	Cys	Asp	Thr	Cys	Phe	Asn	Lys	Asn	Phe	Cys	Thr	Lys	Cys	
	100					105					110					
aaa	agt	gga	ttt	tac	tta	cac	ctt	gga	aag	tgc	ctt	gac	aat	tgc	cca	680
Lys	Ser	Gly	Phe	Tyr	Leu	His	Leu	Gly	Lys	Cys	Leu	Asp	Asn	Cys	Pro	
115					120					125					130	
gaa	ggg	ttg	gaa	gcc	aac	aac	cat	act	atg	gag	tgt	gtc	agt	att	gtg	728
Glu	Gly	Leu	Glu	Ala	Asn	Asn	His	Thr	Met	Glu	Cys	Val	Ser	Ile	Val	
				135					140					145		
cac	tgt	gag	gtc	agt	gaa	tgg	aat	cct	tgg	agt	cca	tgc	acg	aag	aag	776
His	Cys	Glu	Val	Ser	Glu	Trp	Asn	Pro	Trp	Ser	Pro	Cys	Thr	Lys	Lys	
			150					155					160			
gga	aaa	aca	tgt	ggc	ttc	aaa	aga	ggg	act	gaa	aca	cgg	gtc	cga	gaa	824
Gly	Lys	Thr	Cys	Gly	Phe	Lys	Arg	Gly	Thr	Glu	Thr	Arg	Val	Arg	Glu	
		165					170					175				
ata	ata	cag	cat	cct	tca	gca	aag	ggg	aac	cta	tgt	ccc	cca	aca	aat	872
Ile	Ile	Gln	His	Pro	Ser	Ala	Lys	Gly	Asn	Leu	Cys	Pro	Pro	Thr	Asn	
	180					185					190					
gag	aca	aga	aag	tgt	aca	gtg	caa	agg	aag	aag	tgt	cag	aag	gga	gaa	920
Glu	Thr	Arg	Lys	Cys	Thr	Val	Gln	Arg	Lys	Lys	Cys	Gln	Lys	Gly	Glu	
195					200					205				210		
cga	gga	aaa	aaa	gga	agg	gag	agg	aaa	aga	aaa	aaa	cct	aat	aaa	gga	968
Arg	Gly	Lys	Lys	Gly	Arg	Glu	Arg	Lys	Arg	Lys	Lys	Pro	Asn	Lys	Gly	
				215					220					225		
gaa	agt	aaa	gaa	gca	ata	cct	gac	agc	aaa	agt	ctg	gaa	tcc	agc	aaa	1016
Glu	Ser	Lys	Glu	Ala	Ile	Pro	Asp	Ser	Lys	Ser	Leu	Glu	Ser	Ser	Lys	
			230					235					240			
gaa	atc	cca	gag	caa	cga	gaa	aac	aaa	cag	cag	cag	aag	aag	cga	aaa	1064
Glu	Ile	Pro	Glu	Gln	Arg	Glu	Asn	Lys	Gln	Gln	Gln	Lys	Lys	Arg	Lys	
		245					250					255				
gtc	caa	gat	aaa	cag	aaa	tcg	gta	tca	gtc	agc	act	gta	cac	tag		1109
Val	Gln	Asp	Lys	Gln												

<210> 10
 <211> 272
 <212> PRT
 <213> Homo sapiens

<400> 10

Met His Leu Arg Leu Ile Ser Trp Leu Phe Ile Ile Leu Asn Phe Met
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Glu Tyr Ile Gly Ser Gln Asn Ala Ser Arg Gly Arg Arg Gln Arg Arg
 20 25 30

Met His Pro Asn Val Ser Gln Gly Cys Gln Gly Gly Cys Ala Thr Cys
 35 40 45

Ser Asp Tyr Asn Gly Cys Leu Ser Cys Lys Pro Arg Leu Phe Phe Ala
 50 55 60

Leu Glu Arg Ile Gly Met Lys Gln Ile Gly Val Cys Leu Ser Ser Cys
 65 70 75 80

Pro Ser Gly Tyr Tyr Gly Thr Arg Tyr Pro Asp Ile Asn Lys Cys Thr
 85 90 95

Lys Cys Lys Ala Asp Cys Asp Thr Cys Phe Asn Lys Asn Phe Cys Thr
 100 105 110

Lys Cys Lys Ser Gly Phe Tyr Leu His Leu Gly Lys Cys Leu Asp Asn
 115 120 125

Cys Pro Glu Gly Leu Glu Ala Asn Asn His Thr Met Glu Cys Val Ser
 130 135 140

Ile Val His Cys Glu Val Ser Glu Trp Asn Pro Trp Ser Pro Cys Thr
 145 150 155 160

Lys Lys Gly Lys Thr Cys Gly Phe Lys Arg Gly Thr Glu Thr Arg Val
 165 170 175

Arg Glu Ile Ile Gln His Pro Ser Ala Lys Gly Asn Leu Cys Pro Pro
 180 185 190

Thr Asn Glu Thr Arg Lys Cys Thr Val Gln Arg Lys Lys Cys Gln Lys
 195 200 205

Gly Glu Arg Gly Lys Lys Gly Arg Glu Arg Lys Arg Lys Lys Pro Asn
 210 215 220

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Lys Gly Glu Ser Lys Glu Ala Ile Pro Asp Ser Lys Ser Leu Glu Ser
225 230 235 240

Ser Lys Glu Ile Pro Glu Gln Arg Glu Asn Lys Gln Gln Gln Lys Lys
245 250 255

Arg Lys Val Gln Asp Lys Gln Lys Ser Val Ser Val Ser Thr Val His
260 265 270

<210> 11
<211> 819

<212> DNA
<213> Homo sapiens

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tgccaaggag gctgtgcaac atgctcagat tacaatggat gtttgtcatg taagcccaga 180
ctattttttg ctctggaaag aattggcatg aagcagattg gagtatgtct ctcttcattg 240
ccaagtggat attatggaac tcgatatcca gatataaata agtgtacaaa atgcaaagct 300
gactgtgata cctgtttcaa caaaaatttc tgcacaaaat gtaaaagtgg attttactta 360
caccttgga agtgccttga caattgcccc gaagggttgg aagccaacaa ccatactatg 420
gagtgtgtca gtattgtgca ctgtgaggtc agtgaatgga atccttggag tccatgcacg 480
aagaagggaa aaacatgtgg cttcaaaaga gggactgaaa cacgggtccg agaaataata 540
cagcatcctt cagcaaaggg taacctatgt cccccaacaa atgagacaag aaagtgtaca 600
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aaaaaaccta ataaaggaga aagtaaagaa gcaatacctg acagcaaaag tctggaatcc 720
agcaaagaaa tcccagagca acgagaaaac aaacagcagc agaagaagcg aaaagtccaa 780
gataaacaga aatcggtatc agtcagcact gtacactag 819

<210> 12
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<212> DNA
<213> Homo sapiens

<220>
<221> CDS

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 245 250 255

aag cga aaa gtc caa gat aaa cag aaa tcg gta tca gtc agc act gta 816
 Lys Arg Lys Val Gln Asp Lys Gln Lys Ser Val Ser Val Ser Thr Val
 260 265 270

cac tag 822
 His

<210> 13
 <211> 273

<212> PRT
 <213> Homo sapiens

<400> 13

Met Gly His Leu Arg Leu Ile Ser Trp Leu Phe Ile Ile Leu Asn Phe
 1 5 10 15

Met Glu Tyr Ile Gly Ser Gln Asn Ala Ser Arg Gly Arg Arg Gln Arg
 20 25 30

Arg Met His Pro Asn Val Ser Gln Gly Cys Gln Gly Gly Cys Ala Thr
 35 40 45

Cys Ser Asp Tyr Asn Gly Cys Leu Ser Cys Lys Pro Arg Leu Phe Phe
 50 55 60

Ala Leu Glu Arg Ile Gly Met Lys Gln Ile Gly Val Cys Leu Ser Ser
 65 70 75 80

Cys Pro Ser Gly Tyr Tyr Gly Thr Arg Tyr Pro Asp Ile Asn Lys Cys
 85 90 95

Thr Lys Cys Lys Ala Asp Cys Asp Thr Cys Phe Asn Lys Asn Phe Cys
 100 105 110

Thr Lys Cys Lys Ser Gly Phe Tyr Leu His Leu Gly Lys Cys Leu Asp
 115 120 125

Asn Cys Pro Glu Gly Leu Glu Ala Asn Asn His Thr Met Glu Cys Val
 130 135 140

Ser Ile Val His Cys Glu Val Ser Glu Trp Asn Pro Trp Ser Pro Cys
 145 150 155 160

Thr Lys Lys Gly Lys Thr Cys Gly Phe Lys Arg Gly Thr Glu Thr Arg
 165 170 175

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Val Arg Glu Ile Ile Gln His Pro Ser Ala Lys Gly Asn Leu Cys Pro
180 185 190

Pro Thr Asn Glu Thr Arg Lys Cys Thr Val Gln Arg Lys Lys Cys Gln
195 200 205

Lys Gly Glu Arg Gly Lys Lys Gly Arg Glu Arg Lys Arg Lys Lys Pro
210 215 220

Asn Lys Gly Glu Ser Lys Glu Ala Ile Pro Asp Ser Lys Ser Leu Glu
225 230 235 240

Ser Ser Lys Glu Ile Pro Glu Gln Arg Glu Asn Lys Gln Gln Gln Lys
245 250 255

Lys Arg Lys Val Gln Asp Lys Gln Lys Ser Val Ser Val Ser Thr Val
260 265 270

His

<210> 14

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<212> PRT

<213> Homo sapiens

<400> 14

Cys Thr Lys Cys Lys Ala Asp Cys Asp Thr Cys Phe Asn Lys Asn Phe
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Cys Thr Lys Cys Lys Ser Gly Phe Tyr Leu His Leu Gly Lys Cys Leu
20 25 30

Asp Asn Cys Pro Glu Gly Leu Glu Ala Asn Asn His Thr Met Glu Cys
35 40 45

Val Ser Ile Val His Cys Glu Val Ser Glu Trp Asn Pro Trp Ser Pro
50 55 60

Cys Thr Lys Lys Gly Lys Thr Cys Gly Phe Lys Arg Gly Thr Glu Thr
65 70 75 80

Arg Val Arg Glu Ile Ile Gln His Pro Ser Ala Lys Gly Asn Leu Cys
85 90 95

Pro Pro Thr Asn Glu Thr Arg Lys Cys Thr Val Gln Arg Lys Lys Cys
100 105 110

Gln Lys Gly Glu Arg Gly Lys Lys Gly Arg Glu Arg Lys Arg Lys Lys
115 120 125

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Pro Asn Lys Gly Glu Ser Lys Glu Ala Ile Pro Asp Ser Lys Ser Leu
130 135 140

Glu Ser Ser Lys Glu Ile Pro Glu Gln Arg Glu Asn Lys Gln Gln Gln
145 150 155 160

<210> 15

<211> 21

<212> PRT

<213> Homo sapiens

<400> 15

Met His Leu Arg Leu Ile Ser Trp Leu Phe Ile Ile Leu Asn Phe Met
1 5 10 15

Glu Tyr Ile Gly Ser

20

<210> 16

<211> 251

<212> PRT

<213> Homo sapiens

<400> 16

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20 25 30

Cys Leu Ser Cys Lys Pro Arg Leu Phe Phe Ala Leu Glu Arg Ile Gly
35 40 45

Met Lys Gln Ile Gly Val Cys Leu Ser Ser Cys Pro Ser Gly Tyr Tyr
50 55 60

Gly Thr Arg Tyr Pro Asp Ile Asn Lys Cys Thr Lys Cys Lys Ala Asp
65 70 75 80

Cys Asp Thr Cys Phe Asn Lys Asn Phe Cys Thr Lys Cys Lys Ser Gly
85 90 95

Phe Tyr Leu His Leu Gly Lys Cys Leu Asp Asn Cys Pro Glu Gly Leu
100 105 110

Glu Ala Asn Asn His Thr Met Glu Cys Val Ser Ile Val His Cys Glu
115 120 125

Val Ser Glu Trp Asn Pro Trp Ser Pro Cys Thr Lys Lys Gly Lys Thr
130 135 140

Cys Gly Phe Lys Arg Gly Thr Glu Thr Arg Val Arg Glu Ile Ile Gln
145 150 155 160

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His Pro Ser Ala Lys Gly Asn Leu Cys Pro Pro Thr Asn Glu Thr Arg
165 170 175

Lys Cys Thr Val Gln Arg Lys Lys Cys Gln Lys Gly Glu Arg Gly Lys
180 185 190

Lys Gly Arg Glu Arg Lys Arg Lys Lys Pro Asn Lys Gly Glu Ser Lys
195 200 205

Glu Ala Ile Pro Asp Ser Lys Ser Leu Glu Ser Ser Lys Glu Ile Pro
210 215 220

Glu Gln Arg Glu Asn Lys Gln Gln Gln Lys Lys Arg Lys Val Gln Asp
225 230 235 240

Lys Gln Lys Ser Val Ser Val Ser Thr Val His
245 250

<210> 17

<211> 23

<212> PRT

<213> Homo sapiens

<400> 17

Ala Asp Cys Asp Thr Cys Phe Asn Lys Asn Phe Cys Thr Lys Cys Lys
1 5 10 15

Ser Gly Phe Tyr Leu His Leu
20

<210> 18

<211> 46

<212> PRT

<213> Homo sapiens

<400> 18

Ile Asn Lys Cys Thr Lys Cys Lys Ala Asp Cys Asp Thr Cys Phe Asn
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Lys Asn Phe Cys Thr Lys Cys Lys Ser Gly Phe Tyr Leu His Leu Gly
20 25 30

Lys Cys Leu Asp Asn Cys Pro Glu Gly Leu Glu Ala Asn Asn
35 40 45

<210> 19

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<212> PRT

<213> Homo sapiens

<400> 19

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<400> 23

Thr Cys Phe Asn Lys Asn Phe Cys Thr Lys Cys Lys Ser Gly
1 5 10

<210> 24

<211> 20

<212> PRT

<213> Homo sapiens

<400> 24

Cys Glu Val Ser Glu Trp Asn Pro Trp Ser Pro Cys Thr Lys Lys Gly
1 5 10 15

Lys Thr Cys Gly
20

<210> 25

<211> 229

<212> PRT

<213> Mus musculus

<400> 25

Val Gly Ser Arg Gly Ile Lys Gly Lys Arg Gln Arg Arg Ile Ser Ala
1 5 10 15

Glu Gly Ser Gln Ala Cys Ala Lys Gly Cys Glu Leu Cys Ser Glu Val
20 25 30

Asn Gly Cys Leu Lys Cys Ser Pro Lys Leu Phe Ile Leu Leu Glu Arg
35 40 45

Asn Asp Ile Arg Gln Val Gly Val Cys Leu Pro Ser Cys Pro Pro Gly
50 55 60

Tyr Phe Asp Ala Arg Asn Pro Asp Met Asn Lys Cys Ile Lys Cys Lys
65 70 75 80

Ile Glu His Cys Glu Ala Cys Phe Ser His Asn Phe Cys Thr Lys Cys
85 90 95

Gln Glu Ala Leu Tyr Leu His Lys Gly Arg Cys Tyr Pro Ala Cys Pro
100 105 110

Glu Gly Ser Thr Ala Ala Asn Ser Thr Met Glu Cys Gly Ser Pro Ala
115 120 125

Gln Cys Glu Met Ser Glu Trp Ser Pro Trp Gly Pro Cys Ser Lys Lys
130 135 140

Arg Lys Leu Cys Gly Phe Arg Lys Gly Ser Glu Glu Arg Thr Arg Arg
145 150 155 160

Val Leu His Ala Pro Gly Gly Asp His Thr Thr Cys Ser Asp Thr Lys
165 170 175

00004912 062301

09897E 060307

<400> 26

16

Lys Gly Glu Ser Lys Glu Ala Ile Pro Asp Ser Lys Ser Leu Glu Ser
225 230 235 240

Ser Lys Glu Ile Pro Glu Gln Arg Glu Asn Lys Gln Gln Gln Lys Lys
245 250 255

Arg Lys Val Gln Asp Lys Gln Lys Ser
260 265

<210> 27
<211> 8
<212> PRT
<213> Homo sapiens

<400> 27
Ser Val Ser Val Ser Thr Val His
1 5

<210> 28
<211> 7
<212> PRT
<213> Homo sapiens

<400> 28
Val Ser Val Ser Thr Val His
1 5

<210> 29
<211> 27
<212> PRT
<213> Homo sapiens

<400> 29
Gly Ile Glu Val Thr Leu Ala Glu Gly Leu Thr Ser Val Ser Gln Arg
1 5 10 15

Thr Gln Pro Thr Pro Cys Arg Arg Arg Tyr Leu
20 25

<210> 30
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 30
ctcgggaaga agcgcgccat ttgtgttggt

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<210> 31
<211> 2384
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (511)..(1347)

<400> 31

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gccgctgcag cctctgagcc ccaggggcca ctgctcgcct ggattccgcc cgcagccgcc 180
gctgctgtgc aaccgaggct aacctgcggc cagccaggag gctcctgcaa ccttcgctcg 240
cggcgatgac agccacccca gagcagccgg ctgtgttcgg acaatttgag aatgcaattg 300
ttggtttccc ggtccacccg tcccgttcg ctgtccatca cagcacgcct gttggatctc 360
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catacatatt tttctttaaa aaaaaacatt aaatataact aacagtgaaa agaaaaagga 480
gagaaaaaag ggaaacatta caggggttact atg cac ttg cga ctg att tct tgt 534
                               1             5
                               Met His Leu Arg Leu Ile Ser Cys

ttt ttt atc att ttg aac ttt atg gaa tac att ggc agc caa aac gcc 582
Phe Phe Ile Ile Leu Asn Phe Met Glu Tyr Ile Gly Ser Gln Asn Ala
      10              15              20

tcc cga gga agg cgc cag cga aga atg cat cct aat gtc agt caa ggc 630
Ser Arg Gly Arg Arg Gln Arg Arg Met His Pro Asn Val Ser Gln Gly
      25              30              35              40

tgc caa gga ggc tgt gca acg tgt tca gat tac aat ggc tgt ttg tca 678
Cys Gln Gly Gly Cys Ala Thr Cys Ser Asp Tyr Asn Gly Cys Leu Ser
              45              50              55

tgt aag ccc aga ctg ttt ttt gtt ctg gaa agg att ggc atg aag cag 726
Cys Lys Pro Arg Leu Phe Phe Val Leu Glu Arg Ile Gly Met Lys Gln
              60              65              70

ata gga gtg tgt ctc tct tcg tgt cca agt gga tat tac gga act cga 774
Ile Gly Val Cys Leu Ser Ser Cys Pro Ser Gly Tyr Tyr Gly Thr Arg
      75              80              85

tat cca gat ata aat aaa tgt aca aaa tgc aaa gtt gac tgt gat acc 822
Tyr Pro Asp Ile Asn Lys Cys Thr Lys Cys Lys Val Asp Cys Asp Thr
      90              95              100

tgt ttc aac aaa aat ttc tgc aca aag tgt aaa agt gga ttt tac tta 870
Cys Phe Asn Lys Asn Phe Cys Thr Lys Cys Lys Ser Gly Phe Tyr Leu
     105              110              115              120

cac ctt gga aag tgc ctt gac agt tgc cca gaa ggg tta gaa gcc aac 918
His Leu Gly Lys Cys Leu Asp Ser Cys Pro Glu Gly Leu Glu Ala Asn
              125              130              135

aat cat act atg gaa tgt gtc agt att gta cac tgt gag gcc agt gaa 966
Asn His Thr Met Glu Cys Val Ser Ile Val His Cys Glu Ala Ser Glu
              140              145              150

tgg agt cca tgg agt cca tgt atg aag aaa gga aaa aca tgt ggc ttc 1014
Trp Ser Pro Trp Ser Pro Cys Met Lys Lys Gly Lys Thr Cys Gly Phe
              155              160              165

aaa agg ggg act gaa aca cgg gtc cga gat ata cta cag cat cct tca 1062
Lys Arg Gly Thr Glu Thr Arg Val Arg Asp Ile Leu Gln His Pro Ser
      170              175              180

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gcc aag ggt aag ggt aac ctg tgc ccc cca acc agc gag aca aga act 1110
Ala Lys Gly Lys Gly Asn Leu Cys Pro Pro Thr Ser Glu Thr Arg Thr
185 190 195 200

tgt ata gta caa aga aag aag tgt tca aag gga gag cga gga aaa aag 1158
Cys Ile Val Gln Arg Lys Lys Cys Ser Lys Gly Glu Arg Gly Lys Lys
205 210 215

gga aga gag aga aaa cga aaa aaa ctg aat aaa gaa gaa aga aag gaa 1206
Gly Arg Glu Arg Lys Arg Lys Lys Leu Asn Lys Glu Glu Arg Lys Glu
220 225 230

aca agc tcc tcc tct gac agc aaa ggt ttg gag tcc agc att gag acc 1254
Thr Ser Ser Ser Ser Asp Ser Lys Gly Leu Glu Ser Ser Ile Glu Thr
235 240 245

cca gac cag cag gaa aac aaa gag agg cag cag cag cag aag aga aga 1302
Pro Asp Gln Gln Glu Asn Lys Glu Arg Gln Gln Gln Gln Lys Arg Arg
250 255 260

gcc cga gac aag caa cag aaa tcg gta tca gtc agc act gta cac 1347
Ala Arg Asp Lys Gln Gln Lys Ser Val Ser Val Ser Thr Val His
265 270 275

tagagggtcc tgcgagggtta ctgtagactc atgatgctgc tatctcaacc agatgtccag 1407
gacaggtggt ctagccatta gaaccacaaa tggacaacac atcagttacc actctgtcta 1467
aacaacattc ctaatagttg ctatattctt catacaaaca tagtaaacag caaagagcca 1527
aatgttcaaa gaagggatac tttcagatgg ttatcttatg tgcttctgtg tattttttaa 1587
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gctcagaatt agggcctggc attttgaatc ctagagttaa tcatcacaga agcaagtgg 1887
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aacaaaagtg taagaagaat gtgacatggt tgcaaagttg agtggtttct ttctgaaatg 2247
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taaaaaaaaa aaaaaaa 2384

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<210> 32

<211> 279
 <212> PRT
 <213> Mus musculus

<400> 32

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Met His Leu Arg Leu Ile Ser Cys Phe Phe Ile Ile Leu Asn Phe Met
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Glu Tyr Ile Gly Ser Gln Asn Ala Ser Arg Gly Arg Arg Gln Arg Arg
      20           25           30

Met His Pro Asn Val Ser Gln Gly Cys Gln Gly Gly Cys Ala Thr Cys
      35           40           45

Ser Asp Tyr Asn Gly Cys Leu Ser Cys Lys Pro Arg Leu Phe Phe Val
      50           55           60

Leu Glu Arg Ile Gly Met Lys Gln Ile Gly Val Cys Leu Ser Ser Cys
      65           70           75           80

Pro Ser Gly Tyr Tyr Gly Thr Arg Tyr Pro Asp Ile Asn Lys Cys Thr
      85           90           95

Lys Cys Lys Val Asp Cys Asp Thr Cys Phe Asn Lys Asn Phe Cys Thr
      100          105          110

Lys Cys Lys Ser Gly Phe Tyr Leu His Leu Gly Lys Cys Leu Asp Ser
      115          120          125

Cys Pro Glu Gly Leu Glu Ala Asn Asn His Thr Met Glu Cys Val Ser
      130          135          140

Ile Val His Cys Glu Ala Ser Glu Trp Ser Pro Trp Ser Pro Cys Met
      145          150          155          160

Lys Lys Gly Lys Thr Cys Gly Phe Lys Arg Gly Thr Glu Thr Arg Val
      165          170          175

Arg Asp Ile Leu Gln His Pro Ser Ala Lys Gly Lys Gly Asn Leu Cys
      180          185          190

Pro Pro Thr Ser Glu Thr Arg Thr Cys Ile Val Gln Arg Lys Lys Cys
      195          200          205

Ser Lys Gly Glu Arg Gly Lys Lys Gly Arg Glu Arg Lys Arg Lys Lys
      210          215          220

Leu Asn Lys Glu Glu Arg Lys Glu Thr Ser Ser Ser Ser Asp Ser Lys
      225          230          235          240

Gly Leu Glu Ser Ser Ile Glu Thr Pro Asp Gln Gln Glu Asn Lys Glu
      245          250          255

Arg Gln Gln Gln Gln Lys Arg Arg Ala Arg Asp Lys Gln Gln Lys Ser
      260          265          270

Val Ser Val Ser Thr Val His
      275

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<210> 33
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21

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22

<213> Homo sapiens

<400> 34

Met His Leu Arg Leu Ile Ser Trp Leu Phe Ile Ile Leu Asn Phe Met
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Met His Pro Asn Val Ser Gln Gly Cys Gln Gly Gly Cys Ala Thr Cys
35 40 45

Ser Asp Tyr Asn Gly Cys Leu Ser Cys Lys Pro Arg Leu Phe Phe Ala
50 55 60

Leu Glu Arg Ile Gly Met Lys Gln Ile Gly Val Cys Leu Ser Ser Cys
65 70 75 80

Pro Ser Gly Tyr Tyr Gly Thr Arg Tyr Pro Asp Ile Asn Lys Cys Thr
85 90 95

Lys Cys Lys Ala Asp Cys Asp Thr Cys Phe Asn Lys Asn Phe Cys Thr
100 105 110

Lys Cys Lys Ser Gly Phe Tyr Leu His Leu Gly Lys Cys Leu Asp Asn
115 120 125

Cys Pro Glu Gly Leu Glu Ala Asn Asn His Thr Met Glu Cys Val Ser
130 135 140

Ile Val His Cys Glu Val Ser Glu Trp Asn Pro Trp Ser Pro Cys Thr
145 150 155 160

Lys Lys Gly Lys Thr Cys Gly Phe Lys Arg Gly Thr Glu Thr Arg Val
165 170 175

Arg Glu Ile Ile Gln His Pro Ser Ala Lys Gly Asn Leu Cys Pro Pro
180 185 190

Thr Asn Glu Thr Arg Lys Cys Thr Val Gln Arg Lys Lys Cys Gln Lys
195 200 205

Gly Glu Arg Gly Lys Lys Gly Arg Glu Arg Lys Arg Lys Lys Pro Asn
210 215 220

Lys Gly Glu Ser Lys Glu Ala Ile Pro Asp Ser Lys Ser Leu Glu Ser
225 230 235 240

Ser Lys Glu Ile Pro Glu Gln Arg Glu Asn Lys Gln Gln Gln Lys Lys
245 250 255

Arg Lys Val Gln Asp Lys Gln Lys Ser Val Ser Val Ser Thr Val His
260 265 270

<210> 35

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

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<400> 37
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<400> 38
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<400> 39
agcagcgcta tcggatgtga gaggagaagt 30

<400> 40
ctattaacaa atatatttat tgtgggtggct 30

<210> 41
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 41
tggtggcttt ctcccctact agatatacct 30

<210> 42
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 42
gatttttaggt gacactatag 20

<210> 43
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 43
ccgctcgagc caccatgcac ttgcgactga tttc 34

<210> 44
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 44
attgaattcc tagtgtacag tgctgactg 29

<210> 45
<211> 84
<212> DNA
<213> Homo sapiens

<220>
<223> Description of Artificial Sequence: PCR primer

<220>
<221> CDS
<222> (1)..(81)

<400> 45,

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tgcaggagga ggtatctctg agtgtgcagc acagaatcgc atgaccacc ttaaccttcc 1200
tgttgatcatg gaaggatgca cggctgctct gtccactgtg attcctagcc ctctcaagat 1260
cactgctttc tgaagaattt gcaatgactc tggcttctgg ctgcttatct ctggacaccc 1320
gttctccacc agttgtacag ttcattgtaat ctacttggct taattgattt tccacttctc 1380
tcttctcttt ctaagatata aacatttttaa atgatttaaa aaaaaaaaaa aaaaaa 1436

<210> 48
<211> 292
<212> PRT
<213> Homo sapiens

<400> 48
Met His Leu Arg Leu Ile Ser Trp Leu Phe Ile Ile Leu Asn Phe Met
1 5 10 15
Glu Tyr Ile Gly Ser Gln Asn Ala Ser Arg Gly Arg Arg Gln Arg Arg
20 25 30
Met His Pro Asn Val Ser Gln Gly Cys Gln Gly Gly Cys Ala Thr Cys
35 40 45
Ser Asp Tyr Asn Gly Cys Leu Ser Cys Lys Pro Arg Leu Phe Phe Ala
50 55 60
Leu Glu Arg Ile Gly Met Lys Gln Ile Gly Val Cys Leu Ser Ser Cys
65 70 75 80
Pro Ser Gly Tyr Tyr Gly Thr Arg Tyr Pro Asp Ile Asn Lys Cys Thr
85 90 95
Lys Cys Lys Ala Asp Cys Asp Thr Cys Phe Asn Lys Asn Phe Cys Thr
100 105 110
Lys Cys Lys Ser Gly Phe Tyr Leu His Leu Gly Lys Cys Leu Asp Asn
115 120 125
Cys Pro Glu Gly Leu Glu Ala Asn Asn His Thr Met Glu Cys Val Ser
130 135 140
Ile Val His Cys Glu Val Ser Glu Trp Asn Pro Trp Ser Pro Cys Thr
145 150 155 160
Lys Lys Gly Lys Thr Cys Gly Phe Lys Arg Gly Thr Glu Thr Arg Val
165 170 175
Arg Glu Ile Ile Gln His Pro Ser Ala Lys Gly Asn Leu Cys Pro Pro
180 185 190
Thr Asn Glu Thr Arg Lys Cys Thr Val Gln Arg Lys Lys Cys Gln Lys
195 200 205
Gly Glu Arg Gly Lys Lys Gly Arg Glu Arg Lys Arg Lys Lys Pro Asn
210 215 220

06541912.062801

See
at
cont

Lys Gly Glu Ser Lys Glu Ala Ile Pro Asp Ser Lys Ser Leu Glu Ser
225 230 235 240

Ser Lys Glu Ile Pro Glu Gln Arg Glu Asn Lys Gln Gln Gln Lys Lys
245 250 255

Arg Lys Val Gln Asp Lys Gln Lys Ser Gly Ile Glu Val Thr Leu Ala
260 265 270

Glu Gly Leu Thr Ser Val Ser Gln Arg Thr Gln Pro Thr Pro Cys Arg
275 280 285

Arg Arg Tyr Leu
290

full
a
cont

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